

Genotypic and phenotypic characterization of different probiotic strains of *Lactobacillus* spp. and *Bifidobacterium* spp.

Silvino S. Henriques, Guilherme M. Ribeiro, Marta W. Vasconcelos, Ana Gomes

Escola Superior de Biotecnologia, Universidade Católica Portuguesa
Rua Dr. António Bernardino Almeida, P-4200-072 Porto, Portugal

The probiotics' beneficial effects on human health are well documented. One of such benefits is the capacity of certain probiotic strains to decrease serum cholesterol levels in the presence of bile salts. This is done via the activity of the enzyme bile salt hydrolase (BSH). At the present study, three bile salts were tested: glycocholate, taurocholate and taurodeoxycholate. Glycocholate induced the highest specific activities, and activity was strongly strain dependent: *B. animalis* Bb12 showed the lowest activity, whereas *L. acidophilus* L10, *L. pentosus* LMG 10755 and *L. brevis* LMG 6906 showed the highest activity. Another enzyme, conjugated linoleic acid (CLA) isomerase, was object of study because of its beneficial health effects associated with the conversion of linoleic acid into its conjugated forms. Both ewe and goat fermented milk induced rising CLA values in the presence of probiotics, in particular by *B. animalis* strains. No significant differences between matrixes were detected.

Bioinformatic and PCR analysis using orthologous primers were conducted in order to evaluate the effect of genetic similarities and enzymatic activities. The data suggested a strong evolutionary relationship between sequences, probably due genetic conservation amongst different probiotic species and strains. Similarities between genotypic and phenotypic analysis were found, but for the most part detection of the gene and/or evolutionary closeness did not correlate with enzymatic activities. PCR of CLA detected the gene on most *Lactobacillus* species tested. Two strains of *B. animalis* and one strain of *L. acidophilus* on which this gene was detected induced CLA production.

Other genes related to probiotic features were genotypically accessed, namely adhesins and mucin-binding proteins, which establish the ability to colonize and to provide antagonistic effects against pathogens. Again, PCR using orthologous primers suggested evolutionary relatedness. In this work we will present the above mentioned biochemical parameters, and will discuss the relationship and the potential of different methods to detect probiotic features.